

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2003, 16:23:48 ; Search time 48.0429 Seconds
(without alignments)
102.055 Million cell updates/sec

Title: US-09-905-691-3

Perfect score: 19

Sequence: 1 AEARARARARARARARA 19

Scoring table: OLIGO

Gapop 60.0 , Gapert 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	9	47.4	2027	12 Q91TW9	Q91tw9 maize rayad
2	8	42.1	127	2 Q8G161	Q8g161 terrabacter
3	8	42.1	144	17 Q9XD73	Q9yd73 aeropyrum p
4	8	42.1	187	10 Q8H4F3	Q8h4f3 oryza sativ
5	8	42.1	238	4 Q8ND94	Q8nd94 homo sapien
6	8	42.1	284	16 Q69835	Q69835 streptomyc
7	8	42.1	292	2 P72842	P72842 streptomyc
8	8	42.1	327	2 Q30370	Q30370 pseudomonas
9	8	42.1	328	16 Q91LL5	Q91ll5 pseudomonas
10	8	42.1	334	16 Q930Q4	Q930q4 rhizobium m
11	8	42.1	485	16 Q912L1	Q912l1 streptomyc
12	8	42.1	493	5 Q965Y4	Q965y4 caenorhabdi
13	8	42.1	501	16 Q92C02	Q92c02 streptomyc
14	8	42.1	507	16 Q8FT37	Q8ft37 corynebacte
15	8	42.1	514	3 Q8X0Q3	Q8x0q3 neurospora
16	8	42.1	524	2 Q9AF05	Q9af05 frankia sp.

17	8	42.1	532	16 Q9AA46	Q9aa46 caulobacter
18	8	42.1	1178	10 Q942T3	Q942t3 oryza sativ
19	7	36.8	57	16 Q9K7H8	Q9k7h8 bacillus ha
20	7	36.8	61	9 Q8W608	Q8w6u8 bacterioph
21	7	36.8	71	16 Q8U8Q2	Q8u8q2 agrobacteri
22	7	36.8	84	12 Q8VA48	Q8va48 hepatitis c
23	7	36.8	85	16 Q8FU31	Q8fu31 corynebacte
24	7	36.8	86	10 Q9FVH9	Q9fth9 oryza sativ
25	7	36.8	91	16 Q9A367	Q9a367 caulobacter
26	7	36.8	104	16 Q8FLW2	Q8flw2 corynebacte
27	7	36.8	107	16 Q8NTT7	Q8ntt7 corynebacte
28	7	36.8	112	12 Q81685	Q81685 hepatitis c
29	7	36.8	116	8 Q4NL0	Q9anl0 pleuricospo
30	7	36.8	118	2 Q93HL1	Q93hl1 streptomyc
31	7	36.8	119	10 Q8S2P8	Q8s2p8 oryza sativ
32	7	36.8	125	12 Q8JRG0	Q8jrg0 hepatitis c
33	7	36.8	130	12 Q8JRF9	Q8jrf9 hepatitis c
34	7	36.8	149	3 Q92354	Q92354 schizosacch
35	7	36.8	149	3 Q74884	Q74884 schizosacch
36	7	36.8	157	10 Q8W322	Q8w322 oryza sativ
37	7	36.8	159	8 Q95BP0	Q95bp0 pleuricospo
38	7	36.8	164	10 Q943B9	Q943b9 oryza sativ
39	7	36.8	168	16 Q69907	Q69907 streptomyc
40	7	36.8	183	10 Q94J98	Q94j98 oryza sativ
41	7	36.8	192	12 Q8B8T7	Q8b8t7 human adeno
42	7	36.8	195	10 Q8H8V3	Q8h8v3 oryza sativ
43	7	36.8	200	2 Q9FCN7	Q9fcn7 rhizobium l
44	7	36.8	212	12 Q11344	Q11344 molluscum c
45	7	36.8	216	16 Q93J99	Q93j99 streptomyc

ALIGNMENTS

RESULT 1

Q91TW9 PRELIMINARY; PRD; 2027 AA.
ID Q91TW9
AC Q91TW9;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Polyprotein.
OS Maize rayado fino virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Marafivirus.
OX NCBI_TaxID=59749;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Costa Rican;
RX MEDLINE=21186348; PubMed=11289816;
RA Hammond R.W., Ramirez P.;
RT "Molecular characterization of the genome of maize rayado fino virus, the type member of the genus Marafivirus.";
RL Virology 282:338-347(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Costa Rican;
RA Hammond R.W., Ramirez P., Tounignant M.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF265566; AAK52838.1; -;
DR MEROPS; C21.001; -;
DR InterPro; IPR001788; RNA_dep_RNAPol2.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR InterPro; IPR000574; Tymo_coat.
DR InterPro; IPR000606; Viral_helicase1.
DR Pfam; PF00978; RNA_dep_RNAPol2; 1.
DR Pfam; PF00983; Tymo_coat; 1.
DR Pfam; PF01443; Viral_helicase1; 1.
DR PROSITE; PSS0507; RDRP_POSITIVE; 1.
DR PROSITE; PSS0521; RDRP_VIRAL; 1.
SQ SEQUENCE 2027 AA; 223736 MW; 77B46DC9950B0BF7 CRC64;

Query Match

47.4%; Score 9; DB 12; Length 2027;

Matches	9	Conservative	0	Mismatches	0	Indels	0	Gaps	0
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QY 4 RARRAARA 12
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Db 609 RARRAARA 617

RESULT 2

Q8GI61
ID Q8GI61 PRELIMINARY; PRT; 127 AA.

AC	Q8G1G1;	01-MAR-2003 (T-EMBLrel. 23, Created)
DT		DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT		DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DT		DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE		Hypothetical protein.
DE		Terrabacter sp. DBP63.
OC		Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC		Micrococcales; Intrasporangiales; Terrabacter.
OX		NCBI_TaxID=150395;
OX		NCBI_TaxID=150395;

RN	[1]
RP	SEQUENCE FROM N.A.

RC STRAIN-DBF63;
RA Habe H., Miyakoshi M., Kasuga K., Yoshida T., Nojiri H., Omori T.;
RT "Phthalate catabolic gene cluster is linked to the angular dioxygenase
RT gene in *Terrabacter* sp. strain DBF63";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB084235; BAC54158.1; -.
KW Hypothetical protein.
SQ SEQUENCE 127 AA; 13364 MW; 32979994948814EB CRC64;

Query Match 42.1%; Score 8; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 21;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	10	APARRAA	17
Db	12	APARRAA	19

RESULT 3

Q9YD73
ID Q9YD73 PRELIMINARY; PRT; 144 AA.

AC	Q9YD73;	01-NOV-1999	(TREMBLrel. 12, Created)
DT		01-NOV-1999	(TREMBLrel. 12, Last sequence update)
DT		01-NOV-1999	(TREMBLrel. 12, Last sequence update)
DT		01-MAR-2002	(TREMBLrel. 20, Last annotation update)
DE			Hypothetical protein APE1039.

GN APE1039.
QS *Aeropyrum* pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC Desulfurococcaceae; *Aeropyrum*.
OX NCBI TaxID=56636;

RN	[1]	SEQUENCE FROM N.A.
RP		

STRAIN-K1:
MEDLINE-99310339; PubMed-10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yanazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Anakai A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima T., Tanaka T., Kudoh Y.,
RA Tanakamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT *Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1.*;
RT DNA Res. 6:83-101(1999).

DR EMBL; AP000060; BAA80024.1; -.
KW Hypothetical protein: Complete proteome.

SQ SEQUENCE 144 AA; 14937 MW; 973D6C61A0449375 CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels

Qy	12	AARRAARA	19
Db	3	AARRAARA	10

RESULT 4

Q8H4F3
ID Q8H4F3 PRELIMINARY; PRT; 187 AA.

AC Q8H4R3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE O22013_G04.L3 protein.
GN O22013_G04.L3
AC QJ2013_G04.L3.

05 *Oryza sativa* (japonica cultivar-group).
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OX NCBI_TaxID=39947;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RC Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GAM3); genomic DNA, chromosome 7, BAC
RT clones:QJ231-G04.;
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF004230; BAC20029.1; -.
DR SQR SEQUENCE 187 AA; 20294 MW; 398908C139E3A993 CRC64;

```
Query Match      42.1%; Score 8; DB 10; Length 187;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels
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[illegible]

5f	9	AAAAAA	115
Db	108	BRAAARAA	115

RESULT 5

Q8ND94
ID Q8ND94
PRELIMINARY;
PRT: 238 AA.

AC	Q8ND94:	Created
DT	01-OCT-2002	(TREMBLrel. 22, Last sequence update)
DT	01-OCT-2002	(TREMBLrel. 22, Last sequence update)
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)
DE		Hypothetical protein.

GN DKFZP596G2417.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI TaxId:9606;

RN [1]
RP SEQUENCE FROM N.A.

RC	TISSUE-Uterus	
RA	Koehler K, Beyer A, Meves H.W., Weill B., Wiemann S.;	
RL	Submitted (JUL-2002), to the EMBL/genbank/DBJ databases.	
DR	EMBL; AL834319; CAU39888;1; --	
DR	Interpro; IPR003961; FN_III.	
DR	Pfam; PF00041; fn3; 1.	
DR	SMART; SM00060; FN3; 1.	
KW	Hypothetical protein.	
SQ	SEQUENCE 238 AA; 25262 MW; C7300A7D5A9E3095 CRC64;	

Query Match 42.1%; Score 8; DB 4; Length 238;
Best Local Similarity 100.0%; pred. No. 34;

Matches 8: Conservative: 0: Mismatches 0: Indels 0: Cons

Qy 6 RRAAARAA 13
|||||
Db 228 RRAAARAA 235

RESULT 6

ID 069835 PRELIMINARY; PRT; 284 AA.
 AC 069835;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE ABC-transporter ATP-binding protein.
 GN SC06047 OR SC185.07.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteri; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX Harris D., Taylor K.;
 RA Harris D., Taylor K.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases;
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN-A3(2);
 RA Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN-A3(2);
 RX MEDLINE=9700351; PubMed=8843436;
 RA Redanbach M., Kieser H.M., Denapalte D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmid and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX STRAIN-A3(2) / M145;
 RX MEDLINE=21996410; PubMed=13000953;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitzsch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2)."
 RL Nature 417:141-147(2002).
 DR EMBL; AL939126; CAA18981.1; -;
 DR InterPro; IPR003593; AAA_ATPase.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SM00382; AAA; 1.
 KW ATP-binding; Complete proteome.
 SQ SEQUENCE 284 AA; 30082 MW; BFBD99EC634EA94 CRC64;

Query Match 42.1%; Score 8; DB 16; Length 284;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 RRAAARAA 13
 DB 99 RRAAARAA 106
 |||||

RESULT 7

ID P72542 PRELIMINARY; PRT; 292 AA.
 AC P72542;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

Query Match 42.1%; Score 8; DB 2; Length 327;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 ARAARAA 17
 |||||

DE PapM.
 GN PAPM.
 OS Streptomyces pristinaespiralis.
 OC Bacteria; Actinobacteri; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=38300;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97197164; PubMed=9044253;
 RA Blanc V., Gil P., Bamas-Jacques N., Lorenzon S., Zagorec M.,
 RA Schleuniger J., Bischoff D., Blanche F., Debussche L., Crouzet J.,
 RA Thibaut D.;
 RT "Identification and analysis of genes from Streptomyces
 pristinaespiralis encoding enzymes involved in the biosynthesis of the
 4-dimethylamino-L-phenylalanine precursor of pristinamycin I.";
 RL Mol. Microbiol. 23:191-202(1997).
 DR EMBL; U60417; AAC44869.1; -;
 DR HSSP; P14385; IAQJ.
 DR InterPro; IPR004356; HemK.
 DR InterPro; IPR002052; N6_Mtase.
 DR InterPro; IPR000051; SAM_bind.
 DR TIGRFAMs; TIGR00536; hemK_fam; 1.
 DR PROSITE; PS00092; N6_MTASE; 1.
 SQ SEQUENCE 292 AA; 30850 MW; 7B5A8B8E19F29FC CRC64;

Query Match 42.1%; Score 8; DB 2; Length 292;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 AARAARR 15
 DB 155 AARAARR 162
 |||||

RESULT 8

ID 030370 PRELIMINARY; PRT; 327 AA.
 AC 030370;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PvcA.
 GN PvcA.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-PA01;
 RX MEDLINE=96254009; PubMed=8704959;
 RA Stintzi A., Cornelis P., Hohnadel D., Meyer J.M., Dean C., Poole K.,
 RA Kourambas S., Krishnapillai V.;
 RT "Novel pyoverdine biosynthesis gene(s) of Pseudomonas aeruginosa
 PAO.";
 RL Microbiology 142:1181-1190(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN-PA01;
 RX MEDLINE=99315810; PubMed=10383985;
 RA Stintzi A., Johnson Z., Stonehouse M., Ochshner U., Meyer J.M.,
 RA Vasil M.L., Poole K.;
 RT "The pvc gene cluster of Pseudomonas aeruginosa: role in synthesis of
 the pyoverdine chromophore and regulation by PtxR and pvdS.";
 RL J. Bacteriol. 181:4118-4124(1999).
 DR EMBL; AF002222; AAC21671.1; -;
 SQ SEQUENCE 327 AA; 37019 MW; 08286F3B127C9B8B CRC64;

Query Match 42.1%; Score 8; DB 2; Length 327;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 AARAARR 17
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DB 318 ARAARRAA 325
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RESULT 9
Q911L5 PRELIMINARY; PRT; 328 AA.
AC Q911L5;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Pyoverdine biosynthesis protein pvcA.
GN pvcA OR PA2254.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Coltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
RW EMBL; AE004651; AAG05642.1; -.
KW Complete proteome.
SQ SEQUENCE 328 AA; 37134 MW; DE646CA9BEF43B29 CRC64;

Query Match 42.18; Score 8; DB 16; Length 328;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ARAARRAA 17
|||||
DB 319 ARAARRAA 326

RESULT 10
Q930Q4 PRELIMINARY; PRT; 334 AA.
AC Q930Q4;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Sma0265 protein.
GN Sma0265 OR SMA0265.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396509; PubMed=11481432;
RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
RA Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
RT "Nucleotide sequence and predicted functions of the entire
RT Sinorhizobium meliloti pSymA megaplasmid.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
RW EMBL; AE007208; AAK64799.1; -.
DR InterPro; IPR003767; ldh_2.
DR Pfam; PF02615; ldh_2; 1.
KW Plasmid; Hypothetical protein; Complete proteome.

SQ SEQUENCE 334 AA; 34769 MW; 16E60916304D2F85 CRC64;

Query Match 42.18; Score 8; DB 16; Length 334;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ARARRAAA 10
|||||
DB 306 ARARRAAA 313

RESULT 11
Q9L2L1 PRELIMINARY; PRT; 485 AA.
AC Q9L2L1;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Putative membrane protein.
GN SCO0692 OR SCF42.02C OR SCF42.02C...
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinovitch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
RW EMBL; AL539106; CAB69664.1; -.
KW Complete proteome.
SQ SEQUENCE 485 AA; 50944 MW; 63053A5803396D10 CRC64;

Query Match 42.18; Score 8; DB 16; Length 485;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RAARRAAR 18
|||||
DB 338 RAARRAAR 345

RESULT 12
Q965Y4 PRELIMINARY; PRT; 493 AA.
AC Q965Y4;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Hypothetical protein Y110A2AM.1.
GN Y110A2AM.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
```

RL Science 282:2012-2018(1998).

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RA Smith A.;
RT "The sequence of C. elegans cosmid Y110A2AM.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RA Waterston R.;
RT "Direct Submission."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC024747; AAK85498.1;
DR WormPep; Y110A2AM.1; CE26042.
SQ SEQUENCE 493 AA; 54731 MW; 641ED12E30A26B8D CRC64;

Query Match 42.1%; Score 8; DB 5; Length 493;
Best Local Similarity 100.0%; Pred. No. 52; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

QY 12 AARRAARA 19
DB 178 AARRAARA 185
|||||

RESULT 13

Q9ZC02 PRELIMINARY; PRT; 501 AA.
AC Q9ZC02;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein SCO6511.
GN SCO6511 OR SCIE6.20C.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Seeger K.J., Harris D.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapante D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Harris D.E., Quail M.A., Kieser H.,
RA Thomson N.R., James K.D., Harris D.E., Chandra G., Chen C.W., Collins M.,
RA Harper D., Bateman A., Brown S., Hidalgo J., Hornsby T., Howarth S.,
RA Cronin A., Fraser A., Goble A., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";

RL Nature 417:141-147(2002).
DR EMBL; AL599128; CAA22048.1;
DR InterPro; IPR001206; DAGKC.
DR InterPro; IPR000326; PA_PTPase.
DR Pfam; PF00781; DAGKC; 1.
DR Pfam; PF01569; PAP2; 1.
DR SMART; SM00014; acldppc; 1.
DR SMART; SM00046; DAGKC; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 501 AA; 52342 MW; F124CB7FD5302365 CRC64;

Query Match 42.1%; Score 8; DB 16; Length 501;
Best Local Similarity 100.0%; Pred. No. 63; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

QY 4 RARRAAR 11
DB 71 RARRAAR 78
|||||

RESULT 14

Q8FT37 PRELIMINARY; PRT; 507 AA.
AC Q8FT37;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Conserved hypothetical protein.
GN CE1734.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-IS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RA Kawarabayashi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
RA Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
RA Usuda Y., Sugimoto S.;
RT "The entire genomic sequence of Corynebacterium efficiens YS-314.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005219; BAC18544.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 507 AA; 55464 MW; 5CB3F673AFC7C33A CRC64;

Query Match 42.1%; Score 8; DB 16; Length 507;
Best Local Similarity 100.0%; Pred. No. 63; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

QY 10 ARAARRAA 17
DB 469 ARAARRAA 476
|||||

RESULT 15

Q8X0Q3 PRELIMINARY; PRT; 514 AA.
AC Q8X0Q3;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Conserved hypothetical protein.
GN SE6.140.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte U., Agn V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]

RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL670004; CAD21255.1; -
DR InterPro; IPR007087; znf_C2H2.
DR SMART; SM00355; znf_C2H2; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 514 AA; 57259 MW; F03E63327C2407F3 CRC64;
Query Match 42.1%; Score 8; DB 3; Length 514;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 RAARRAAR 18
| | | | | | | |
Db 232 RAARRAAR 239

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Job time : 50.0429 secs